

**AMENDMENTS TO THE SPECIFICATION**

Page 20

Line 1, please replace page 20 with the following new amended page 20:

**-- Example 2: GENERATING PRIMER SEQUENCES using method as
DESCRIBED -- COMPUTER SIMULATION****(A)**

GENE: AGAMOUS
FUNCTION: TRANSCRIPTION FACTOR
DOMAIN: MADS BOX

<u>SEQ ID NO: 1</u>	AA SEQUENCE:	G R G K I E I K R I E	
<u>SEQ ID NO: 2</u>	Predicted NT:	GGG AGG GGC AAG AUC GAG AUC AAG CGC AUC GAG	
<u>SEQ ID NO: 3</u>	Maize	GGG AGa GGC AAG AUC GAG AUC AAG CGC AUC GAG	32/33
<u>SEQ ID NO: 4</u>	Rice	GGG AGG GGg AAG AUC GAG AUC AAG CGg AUC GAG	31/33
<u>SEQ ID NO: 5</u>	Arabidopsis	GGG AGA GGA AAG AUC GAA AUC AAA CGG AUC GAG	(M) 28/33 (R) 29/33

(B)

GENE: APETALA1
FUNCTION: TRANSCRIPTION FACTOR
DOMAIN: MADS BOX

<u>SEQ ID NO: 6</u>	AA SEQUENCE:	R I E N K I N R EQ V T F	
<u>SEQ ID NO: 7</u>	Predicted NT:	AGG AUC GAG AAC AAG AUC AAC AAG CAG GUG ACC UUC	
<u>SEQ ID NO: 8</u>	Maize	cGG AUC GAG AAC AAG AUC AAC cGG CAG GUg ACC UUC	33/36
<u>SEQ ID NO: 9</u>	Rice	AGG AUC GAG AAC AAG AUC AAC cGG CAG GUG ACg UUC	34/36
<u>SEQ ID NO: 10</u>	Arabidopsis	AGG AUA GAG AAC AAG AUC AAA AGA CAA GUG ACA UUC	(M) 29/36 (R) 30/36

(C)

GENE: APETALA2
FUNCTION: TRANSCRIPTION FACTOR
DOMAIN: AP2 DOMAIN

<u>SEQ ID NO: 11</u>	AA SEQUENCE:	G R W E S H I W D C	
<u>SEQ ID NO: 12</u>	Predicted NT:	GGC AGG UGG GAG UCC CAC AUC UGG GAC UGC	
<u>SEQ ID NO: 13</u>	Maize	GGC cGc UGG GAa UCC CAC AUC UGG GAC UGC	27/30
<u>SEQ ID NO: 14</u>	Arabidopsis	GGA AGA UGG GAA UCU CAU AUU UGG GAC UGU	(M) 23/30 --

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Please replace page 21 with the following new amended page 21:

-- Example 3: SPECIFICITY OF CODON ADJUSTED PRIMERS

The following example illustrates the specificity of codon adjusted primer pairs. Primers 1 and 2 represent primers taken directly from the sequence of the template polynucleotide. Primers 1' and 2' are primers wherein the sequence has been codon adjusted for monocots according to the invention. These primers were used to identify target polynucleotides from corn and rice.

Primer 1

<u>SEQ ID NO: 15</u>	AA SEQUENCE	D C G L Q V
<u>SEQ ID NO: 16</u>	Coding Sequence:	5' G GAC TGT GGG AAA CAA GTT TA 3'
<u>SEQ ID NO: 17</u>	Primer 1 Sequence:	5' G GAC TGT GGG AAA CAA GTT TA 3'

SEQ ID NO: 18 Primer 1' (Codon Adjusted Sequence): 5' G GAC TGC GGG AAG CAG GTG TA 3' 17/21

%Sequence Identity to Primer 1: 81%

Primer 2

<u>SEQ ID NO: 19</u>	AA SEQUENCE	K Y R G V T L
<u>SEQ ID NO: 20</u>	Coding Sequence:	5' AAG TAT AGA GGT GTC ACT TTG CA 3'
<u>SEQ ID NO: 21</u>	Complement	3' TTC ATA TCT CCA CAG TGA AAC GT 5'

SEQ ID NO: 22 Primer 2 Sequence: 5' TG CAA AGT GAC ACC TCT ATA CTT 3'

<u>SEQ ID NO: 23</u>	Codon Adjusted Sequence:	5' AAG TAC AGG GGC GTC ACC TTG CA 3'
<u>SEQ ID NO: 24</u>	Complement	3' TTC ATG TCC CCG CAG TGG AAC GT 5'

SEQ ID NO: 25 Primer 2' Sequence: 5' TG CAA GGT GAC GCC CCT GTA CTT 3' 19/23

%Sequence Identity to Primer 2: 83% --

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Please replace page 23 with the following new amended page 23:

-- Example 4

The method of the invention was used to isolate AP2-like genes from *Avena sativa* (oat), *Oryza sativa* (rice), *Triticum aestivum* (wheat) and *Zea mays* (corn). Primers 1' and 2' described in Example 3 were used in PCR using the conditions of Example 1 and genomic DNA from each plant as a source of target polynucleotides. The nucleotide and corresponding amino acid sequences of PCR-amplified products are shown below.

>OAT ADC GENE 489 BP (SEQ ID NO.: 26)

TACCTAGGTGAGCTCAAATTCACAGCTCCAGCTCCTCCTAATTAATTCCATCTGTTCTGTGTACTGAAGTTATTTAATTTTCGTCAGGTGGTTTCGACACC
GCGCACTCGGCCGCGAGGTTATAATTAATCAAGCTTCCTAGTTTGAAGTTTCAACACATACCTGCTCTCTCGATTGGATTGTACTAGCATCATGAAGTGT
ACTGAAACGGGTCTTGTCTAGGGCTACGATCGCGCGCGCATCAAGTTCCGGGGACTGGACGCCGACATCAACTTCAATCTGAGCGACTACGAGGAGGATC
TGAAGCAGGTAAGTAAGATCGCTTCTCAAATGCAGCATAGATATTATCGGTGTGTGTGTGTCTGATGGGTGGTTGGTGGCCGGCGGGCACTCTTG
TTTTTGCCAGATGAGGAAGTGGACCAAGGAGGAGTTCGTGCACATCTCCGCCGCCAGAGCAGGGGTTTCGCGAGGGGGAGCTCA

>OAT ADC PROTEIN 65 aa (SEQ ID NO: 27)

GGFDTAHSAARAYDRAAIKFRGLDADINFNLSDYEDLKQVTNWTKEEFVHILRRQSTGFARGSS

>RICE AP2-LIKE GENE 387 BP (SEQ ID NO: 28)

CCTAGGTAATTTTCATCGAACACATCATCTTCTCTCTCAATCCAACGCGACATCGCCATGAACAATCTAACAAACACCTTCATCTTCTCCAAACAATCA
CAGGTGGATTTCGACACTGCTCAGCAGCTGCAAGGTAAAGAACACATCACATCATTTCATCAGAATGAGCTCTGTGTTTGTGAAGGAGATTGAGAGAATT
GAATGATGATGGATGGATGACAGGGCGTACGACAGGGCGCGCATCAAGTTTCAGGGGAGTAGAGGCTGACATCAACTTCAACCTGAGCGACTACGAGGAGGAC
ATGAGGCGATGAAGAGCTTGTCCAAGGAGGAGTTCGTGCACGTTCTCCGGCGACAGAGCACCGGCTTCTCCCGCGCGAGCTCA

>RICE ADC PROTEIN 65 aa (SEQ ID NO: 29)

GGFDTAHAAARAYDRAAIKFRGVEADINFNLSDYEDMRQMKSLSKEEFVHVLRRQSTGFSRGSS

>WHEAT ADC GENE 477 BP (SEQ ID NO: 30)

CTTGGGTGGGTTTGACACTGCACATGCTGCTGCAAGGTACGTACAAATTTAATTAAGCACGTACGCAGTACATAATTTGTGATGTGATCATCACCTGAACCA
CCTGTACTGCAACTCTGAAGTTATGTCTCCACTCTGTTTCAATTCACCGTGCCAAATGACCTTGGGATGTTCCGCGAGGGCGTACGATCGAGCGGGCGATCAA
GTTCCGCGGGCTGACGCGGACATAAATTTCAACCTCAGCGACTACGAGGACGACATGAAGCAGGTGATCAGCAAAGCCACCAACAGTGTTCCTCATCCA
ACCAAATATTTCAGATGACAGTGCATTAGTACTGTTGTTGAAACTGATGAACTGAAGAAATTTCTGACTGTGTGTTGTTGGTGGATGATCTGGATCAGAT
GAAGGGCTGTCCAAGGAGGAGTTCGTGCACGTGCTGCGGCGGAGAGCGCCGGCTTCTCGCGGGGAGCTCC

>WHEAT ADC PROTEIN 65 aa (SEQ ID NO: 31)

GGFDTAHAAARAYDRAAIKFRGVDADINFNLSDYEDDMKQVKLSKEEFVHVLRRQSAGFSRGSS

>MAIZE ADC GENE 489 BP (SEQ ID NO: 32)

CTTAGGTGAGCAGCAATAAGCAGATCGATCTGCAGCATAAATTTCCCGTTATTAAGTAGTTTCGTGATCTCGATCGAATGGCCTAATTAACCGATTCCGGTGA
TCTGGCCGATGGCCAATCTACGAGGTGGATTTCGACACTGCTCATGCCGCTGCAAGGTAACGATCAATCCATCCATCCACCTTGTCTAGTACCCCAACCG
ACCGCCGGATTAAATGGACCGCTAGTTCTCGGGACGGGCTTGTCTGAGGGCGTACGACCGAGCGGCGATCAAGTTCCGCGGCGTTCGACGCGGACATAAAT
TCAACCTCAGCGACTACGACGACGATATGAAGCAGGTACATACAGAGTGTGTTGACAGTAGACCGACTGAAACATCTGCTGAACGTACACTCATGGCC
TGTGCACAGATGAAGAGCCTGTCCAAGGAGGAGTTCGTGCACGCCCTGCGGCGGAGAGACCGGCTTCTCCCGTGGCAGCTCC

>MAIZE ADC PROTEIN 65 aa (SEQ ID NO: 33)

GGFDTAHAAARAYDRAAIKFRGVDADINFNLSDYDDMKQVKLSKEEFVHALRRQSTGFSRGSS

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Please replace the paragraph beginning on line 25 with the following new amended paragraph:

--Primer 1

<u>SEQ ID NO: 34</u>	AA SEQUENCE	D C G L Q V
<u>SEQ ID NO: 35</u>	Coding Sequence:	5' G GAC TGT GGG AAA CAA GTT TA 3'
<u>SEQ ID NO: 36</u>	Primer Sequence:	5' G GAC TGT GGG AAA CAA GTT TA 3'
<u>SEQ ID NO: 37</u>	Primer 1' (Codon Adjusted Sequence): 5' G GAC TGC GGG AAG CAG GTG TA 3' --	

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Please replace the paragraph beginning on page 25, line 1 and ending on line 41 with the following new amended paragraph:

-- Primer 2

<u>SEQ ID NO: 38</u>	AA SEQUENCE	K Y R G V T L
<u>SEQ ID NO: 39</u>	Coding Sequence:	5' AAG TAT AGA GGT GTC ACT TTG CA 3'
<u>SEQ ID NO: 40</u>	Complement	3' TTC ATA TCT CCA CAG TGA AAC GT 5'
<u>SEQ ID NO: 41</u>	Primer 2 Sequence:	5' TG CAA AGT GAC ACC TCT ATA CTT 3'
<u>SEQ ID NO: 42</u>	Codon Adjusted Sequence:	5' AAG TAC AGG GGC GTC ACC TTG CA 3'
<u>SEQ ID NO: 43</u>	Complement	3' TTC ATG TCC CCG CAG TGG AAC GT 5'
<u>SEQ ID NO: 44</u>	Primer 2' Sequence:	5' TG CAA GGT GAC GCC CCT GTA CTT 3'
<u>SEQ ID NO: 45</u>	RISZU2'-1 (5 CODONS)	5' G CAA GGT GAC GCC CCT GT 3'
<u>SEQ ID NO: 46</u>	RISZU2'-2 (5 CODONS)	5' GGT GAC GCC CCT GTA CT 3'
<u>SEQ ID NO: 47</u>	RISZU2'-3 (4 CODONS)	5' GT GAC GCC CCT GTA CT 3'
<u>SEQ ID NO: 48</u>	RISZU2'-4 (3 CODONS)	5' GT GAC GCC CCT GT 3' --